



Exhibit 1

- 1 - 82

SEQUENCE LISTING

(1) GENERAL INFORMATION:

T830X

183

- (i) APPLICANTS: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
- (ii) TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
- (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN & FINNEGAN
 - (B) STREET: 345 PARK AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: USA
 - (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/231,565
 - (B) FILING DATE: 22-APR-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: CAROL M. GRUPPI
 - (B) REGISTRATION NUMBER: 37,341
 - (C) REFERENCE/DOCKET NUMBER: 2026-4124
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 758-4800
 - (B) TELEFAX: (212) 751-6849
 - (C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1559
 - (B) TYPE: NUCLEOTIDE
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: UNKNOWN
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAGACAGA GGACTCTCAT TAAGGAAGGT GTCCTGTGCC 40
CTGACCCTAC AAGATGCCAA GAGAAGATGC TCACTTCATC 80
TATGGTTACC CCAAGAAGGG GCACGGCCAC TCTTACACCA 120
CGGCTGAAGA GGCGCTGGG ATCGGCATCC TGACAGTGAT 160
CCTGGGAGTC TTACTGCTCA TCGGCTGTTG GTATTGTAGA 200
AGACGAAATG GATACAGAGC CTTGATGGAT AAAAGTCTTC 240
ATGTTGGCAC TCAATGTGCC TTAACAAGAA GATGCCACAA 280
AGAAGGGTTT GATCATCGGG ACAGCAAAGT GTCTCTTCAA 320
GAGAAAAACT GTGAACCTGT GGTTCCAAT GCTCCACCTG 360
CTTATGAGAA ACTCTCTGCA GAACAGTCAC CACCACCTTA 400
TTCACCTTAA GAGCCAGCGA GACACCTGAG ACATGCTGAA 440
ATTATTTCTC TCACACTTT GCTTGAATT AATACAGACA 480
TCTAATGTTTC TCCTTGAA TGGTGTAGGA AAAATGCAAG 520
CCATCTCTAA TAATAAGTCA GTGTTAAAAT TTTAGTAGGT 560
CCGCTAGCAG TACTAATCAT GTGAGGAAAT GATGAGAAAT 600
ATTAAATTGG GAAAACCCA TCAATAAATG TTGCAATGCA 640
TGATACTATC TGTGCCAGAG GTAATGTTAG TAAATCCATG 680
GTGTTATTTT CTGAGAGACA GAATTCAAGT GGGTATTCTG 720
GGGCCATCCA ATTTCTTTT ACTTGAAATT TGGCTAATAA 760
CAAACTAGTC AGGTTTCGA ACCTTGACCG ACATGAACTG 800
TACACAGAAT TGTTCCAGTA CTATGGAGTG CTCACAAAGG 840
ATACTTTAC AGGTTAAGAC AAAGGGTTGA CTGGCCTATT 880
TATCTGATCA AGAACATGTC AGCAATGTCT CTTTGTGCTC 920
TAAAATTCTA TTATACTACA ATAATATATT GTAAAGATCC 960

*B
Cont.*

TATAGCTCTT	TTTTTTGAG	ATGGAGTTTC	GCTTTGTTG	1000
CCCAGGCTGG	AGTGCAATGG	CGCGATCTTG	GCTCACCATA	1040
ACCTCCGCCT	CCCAGGTTCA	AGCAATTCTC	CTGCCTTAGC	1080
CTCCTGAGTA	GCTGGGATTA	CAGGCGTGCG	CCACTATGCC	1120
TGACTAATTT	TGTAGTTTA	GTAGAGACGG	GGTTTCTCCA	1160
TGTTGGTCAG	GCTGGTCTCA	AACTCCTGAC	CTCAGGTGAT	1200
CTGCCCGCCT	CAGCCTCCCA	AAGTGCTGGA	ATTACAGGCG	1240
TGAGCCACCA	CGCCTGGCTG	GATCCTATAT	CTTAGGTAAG	1280
ACATATAACG	CAGTCTAATT	ACATTTCACT	TCAAGGCTCA	1320
ATGCTATTCT	AACTAATGAC	AAGTATTTTC	TACTAAACCA	1360
GAAATTGGTA	GAAGGATTAA	AATAAGTAAA	AGCTACTATG	1400
TAATGCCTTA	GTGCTGATGC	CTGTGTACTG	CCTTAAATGT	1440
ACCTATGGCA	ATTTAGCTCT	CTTGGGTTCC	CAAATCCCTC	1480
TCACAAGAAT	GTGCAGAAGA	AATCATAAAG	GATCAGAGAT	1520
TCTGAAAAAA	AAAAA	AAAAA	AAAAA	1559

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys
1 5 10

Lys Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala
15 20 25

85
- A -

Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu
30 35 40

Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala
45 50 55

Leu Met Asp Lys Ser Leu His Val Gly Thr Gln Cys Ala Leu
60 65 70

Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg Asp Ser
75 80

Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro
85 90 95

Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110

Pro Pro Pro Tyr Ser Pro
115

b
cm

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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- 5 -

Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Ile Gly Ile Leu Thr Val Ile Leu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ile Leu Thr Val Ile Leu Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ile Leu Thr Val Ile Leu Gly Val Leu
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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cont.
Leu Thr Val Ile Leu Gly Val Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Val Ile Leu Gly Val Leu Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Val Ile Leu Gly Val Leu Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Leu Met Asp Lys Ser Leu His Val
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu His Val Gly Thr Gln Cys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

- 8 -
89

Pro Val Val Pro Asn Ala Pro Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

B
cont.

Asn Ala Pro Pro Ala Tyr Glu Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

90
- 8 -

Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Gly Ile Gly Ile Leu Thr Val Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Ile Leu Thr Val Ile Leu Gly Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Leu Thr Val Ile Leu Gly Val Leu Leu
1 5 10

β
(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Val Ile Leu Gly Val Leu Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Val Ile Leu Gly Val Leu Leu Leu Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Ala Leu Met Asp Lys Ser Leu His Val
1 5 10

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cont
(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Leu His Val Gly Thr Gln Cys Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2172
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTGCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680

TTCTCCGTGA	GCGTGTCCA	GTTGCGGGCC	TTGGATGGAG	720
GGAACAAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760
CCTCCAGCTC	CATGACCCCCA	GTGGCTATCT	GGCTGAAGCT	800
GACCTCTCCT	ACACCTGGGA	CTTTGGAGAC	AGTAGTGGAA	840
CCCTGATCTC	TCGGGCACTT	GTGGTCACTC	ATACTTACCT	880
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920
GCCATTCCCTC	TCACCTCCTG	TGGCTCCTCC	CCAGTTCCAG	960
GCACCACAGA	TGGGCACAGG	CCAACTGCAG	AGGCCCCCTAA	1000
CACCAACAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGCGCC	AACTGCAGAG	CCCTCTGGAA	1080
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120
TGCACCTGTG	CAGATGCCAA	CTGCAGAGAG	CACAGGTATG	1160
ACACCTGAGA	AGGTGCCAGT	TTCAGAGGTC	ATGGGTACCA	1200
CACTGGCAGA	GATGTCAACT	CCAGAGGCTA	CAGGTATGAC	1240
ACCTGCAGAG	GTATCAATTG	TGGTGCTTTC	TGGAACCACA	1280
GCTGCACAGG	TAACAACTAC	AGAGTGGGTG	GAGACCACAG	1320
CTAGAGAGCT	ACCTATCCCT	GAGCCTGAAG	GTCCAGATGC	1360
CAGCTCAATC	ATGTCTACGG	AAAGTATTAC	AGGTTCCCTG	1400
GGCCCCCTGC	TGGATGGTAC	AGCCACCTTA	AGGCTGGTGA	1440
AGAGACAAAGT	CCCCCTGGAT	TGTGTTCTGT	ATCGATATGG	1480
TTCCTTTCC	GTCACCCCTGG	ACATTGTCCA	GGGTATTGAA	1520
AGTGCCGAGA	TCCTGCAGGC	TGTGCCGTCC	GGTGAGGGGG	1560
ATGCATTGAA	GCTGACTGTG	TCCTGCCAAG	GCGGGCTGCC	1600
CAAGGAAGCC	TGCATGGAGA	TCTCATCGCC	AGGGTGCCAG	1640
CCCCCTGCC	AGCGGCTGTG	CCAGCCTGTG	CTACCCAGCC	1680

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Cont.

95

CAGCCTGCCA GCTGGTTCTG CACCA GATAC TGAAGGGTGG 1720
 CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC 1760
 AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG 1800
 GTCAAGAACGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG 1840
 CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG 1880
 ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC 1920
 CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC 1960
 CCGCATCTTC TGCTCTTGTG CCATTGGTGA AACAGCCCC 2000
 CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG 2040
 CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTCC 2080
 CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAAT 2120
 ACTCAGAGCC TGAAAAAAAAA TAAAAAAAAA AAAAAAAAAA 2160
 AAAAAAAAAA AA 2172

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu
 1 5 10

Ala Val Ile Gly Ala Leu Leu Ala Val Gly Ala Thr
 15 20
 Lys Val Pro Arg Asn Gln Asp Trp Leu Gly Val Ser
 25 30 35
 Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu
 40 45
 Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys
 50 55 60
 Trp Arg Gly Gly Gln Val Ser Leu Lys Val Ser Asn
 65 70
 Asp Gly Pro Thr Leu Ile Gly Ala Asn Ala Ser Phe
 75 80
 Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
 85 90 95
 Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr
 100 105
 Ile Ile Asn Gly Ser Gln Val Trp Gly Gly Gln Pro
 110 115 120
 Val Tyr Pro Gln Glu Thr Asp Asp Ala Cys Ile Phe
 125 130
 Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
 135 140
 Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp
 145 150 155
 Gly Gln Tyr Trp Gln Phe Leu Gly Gly Pro Val Ser
 160 165
 Gly Leu Ser Ile Gly Thr Gly Arg Ala Met Leu Gly
 170 175 180
 Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
 185 190
 Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser
 195 200
 Ser Ala Phe Thr Ile Thr Asp Gln Val Pro Phe Ser
 205 210 215
 Val Ser Val Ser Gln Leu Arg Ala Leu Asp Gly Gly
 220 225
 Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe
 230 235 240
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala
 245 250
 Glu Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp
 255 260
 Ser Ser Gly Thr Leu Ile Ser Arg Ala Leu Val Val
 260 265 270
 Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala
 275 280
 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser
 285 290 295
 Cys Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Gly
 300 305
 His Arg Pro Thr Ala Glu Ala Pro Asn Thr Thr Ala
 310 315

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Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
 320 325 330
 Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr
 335 340
 Thr Ser Val Gln Val Pro Thr Thr Glu Val Ile Ser
 345 350 355
 Thr Ala Pro Val Gln Met Pro Thr Ala Glu Ser Thr
 360 365
 Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
 370 375
 Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu
 380 385 390
 Ala Thr Gly Met Thr Pro Ala Glu Val Ser Ile Val
 395 400
 Val Leu Ser Gly Thr Thr Ala Ala Gln Val Thr Thr
 405 410 415
 Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
 420 425
 Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile
 430 435
 Met Ser Thr Glu Ser Ile Thr Gly Ser Leu Gly Pro
 440 445 450
 Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu Val Lys
 455 460
 Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
 465 470 475
 Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly
 480 490
 Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Pro Ser
 495 500
 Gly Glu Gly Asp Ala Phe Glu Leu Thr Val Ser Cys
 505 510 515
 Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
 520 525
 Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu
 530 535 540
 Cys Gln Pro Val Leu Pro Ser Pro Ala Cys Gln Leu
 545 550
 Val Leu His Gln Ile Leu Lys Gly Gly Ser Gly Thr
 555 560
 Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
 565 570 575
 Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly
 580 585
 Gln Glu Ala Gly Leu Gly Gln Val Pro Leu Ile Val
 590 595 600
 Gly Ile Leu Leu Val Leu Met Ala Val Val Leu Ala
 605 610
 Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
 615 620

Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His
625 630 635
Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser Cys Pro
640 645
Ile Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln Gln
650 655 660
Val

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

6
Cmt.
Val Pro Gly Ile Leu Leu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Leu Ser Gly Gln Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Pro Pro Gln Trp Ala Ala Gly Leu Ser Thr Leu Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Leu Asp Gly Gly Asn Lys His Phe Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Leu Lys Arg Cys Leu Leu His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Leu Pro Ser Pro Ala Cys Gln Leu Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Leu Ala Asp Thr Asn Ser Leu Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Val Ser Val Ser Gln Leu Arg Ala
1 5

B
Cmt.
(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Tyr Leu Glu Pro Gly Pro Val Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu Asn Val Ser Leu Ala Asp Thr Asn
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGACAGGCCG AGGCAGGCCTT TTTTTTTTTT TTTTTTTTTT
TTTTTTTTTT TTTTTTTT 40
58

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAATCGCGA CC 12

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGTCGCGATT GGTAA 15

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown

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(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5